Amendments to the Claims

1. (Currently amended) A method for making a hypermutable ~~bacteria~~ bacterium comprising the steps of:

introducing into a bacterium a polynucleotide encoding a form of a PMS2 mismatch repair protein under the control of an inducible transcription regulatory sequence; and

inducing said inducible transcription regulatory sequence in said bacterium; wherein said ~~form of said~~ PMS2 mismatch repair ~~polynucleotide~~ protein exerts a dominant negative effect on mismatch repair when expressed in said bacterium, whereby said bacterium becomes hypermutable.

2-5. (Canceled)

6. (Currently amended) The method of claim 1 wherein the mismatch repair gene is human *PMS2*.

7. (Original) The method of claim 1 wherein the mismatch repair gene is plant *PMS2*.

8-11. (Canceled)

12. (Currently amended) The method of claim ~~3~~ 1 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation.

13. (Canceled)

14. (Previously amended) The method of claim 6 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation.

15. (Previously amended) The method of claim 7 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation.

16. (Currently amended) The method of claim ~~4~~ 7 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation at codon 134.

17. (Previously amended) The method of claim 6 wherein said polynucleotide encoding a form of a mismatch repair protein comprises a truncation mutation at codon 134.

18. (Currently amended) A homogeneous composition of cultured, hypermutable bacteria which comprise a polynucleotide encoding a form of a mismatch repair protein under the control of an inducible transcription regulatory sequence, wherein said mismatch repair protein is a PMS2 mismatch repair protein, wherein said ~~polynucleotide~~ PMS2 mismatch repair protein exerts a dominant negative effect when expressed in said bacteria, and wherein said bacteria are induced.

19-25. (Canceled)

26. (Currently amended) The homogeneous composition of claim ~~20~~ 18 wherein the bacteria express a protein which consists of the first 133 amino acids of PMS2.

27. (Original) The homogeneous composition of claim 26 wherein the protein is human PMS2.

28-70. (Canceled)

71. (Currently amended) The method of claim ~~3~~ 1 wherein the ~~dominant negative allele~~ polynucleotide encoding a form of a PMS2 mismatch repair protein comprises a truncation mutation at codon 134.

72. (New) A method for making a hypermutable bacterium comprising the steps of:

introducing into a bacterium a polynucleotide encoding a form of a mismatch repair protein under the control of an inducible transcription regulatory sequence said mismatch repair protein is selected from the group consisting of a PMSR and a PMS2L mismatch repair protein; and

inducing said bacterium;

wherein said mismatch repair protein exerts a dominant negative effect on mismatch repair when expressed in said bacterium, whereby said bacterium becomes hypermutable.

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73. (New) A homogeneous composition of cultured, hypermutable bacteria which comprise a polynucleotide encoding a form of a mismatch repair protein selected from the group consisting of a PMSR and PMS2L mismatch repair protein under the control of an inducible transcription regulatory sequence, wherein said mismatch repair protein exerts a dominant negative effect when expressed in said bacteria, and wherein said bacteria is induced.